



SEQUENCE LISTING

<110> Seishi KATO
Tomoko KIMURA

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 2003-0986/WMC/01791

<140> 10/019,114

<141> 2000-06-16

<150> JP 11-188835

<151> 1999-07-02

<160> 30

<210> 1

<211> 233

<212> PRT

<213> Homo sapiens

<400> 1

Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu Leu Leu Gly Ser

1 5 10 15

Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn Pro Glu Ala Asn

20 25 30

Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr Pro Tyr Glu Glu

35 40 45

Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly Ile Tyr Arg Ile

50 55 60

Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro Lys Pro Ala Val

65 70 75 80

Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn Trp Ile Cys Asn

85 90 95

Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp Ser Gly Tyr Asp

100 105 110

Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Leu
115 120 125
Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe Ser Leu Asp Glu
130 135 140
Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe Ile Ile Glu Lys
145 150 155 160
Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser Gln Gly Thr Thr
165 170 175
Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu Ala Lys Lys Ile
180 185 190
Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val Lys Tyr Thr Gln
195 200 205
Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg Val Val Lys Val
210 215 220
Cys Asp Phe Pro Ser Phe Asn Leu Lys
225 230

<210> 2
<211> 273
<212> PRT
<213> Homo sapiens

<400> 2

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
1 5 10 15
Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
20 25 30
Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
35 40 45
Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
50 55 60
Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
65 70 75 80
Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
85 90 95

Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
 100 105 110
 Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
 115 120 125
 Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
 130 135 140
 Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
 145 150 155 160
 Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
 165 170 175
 Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
 180 185 190
 Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
 195 200 205
 Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
 210 215 220
 Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
 225 230 235 240
 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln
 245 250 255
 Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
 260 265 270

Ser

<210> 3
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 3

Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu
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 Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro
 20 25 30
 Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu
 35 40 45

Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr Leu Thr
 50 55 60
 Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys
 65 70 75 80
 Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp
 85 90 95
 Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala
 100 105 110
 Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys
 115 120 125
 Arg Ser Glu Asn Lys Asn Glu Gly Gln Asp Ala Thr Met Tyr Cys Lys
 130 135 140
 Ser Val Gly Tyr Pro His Pro Asp Trp Ile Trp Arg Lys Lys Glu Asn
 145 150 155 160
 Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe Ile Ile
 165 170 175
 Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln Ile Thr
 180 185 190
 Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile Gly Ser
 195 200 205
 Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala Pro Leu
 210 215 220
 Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val Val Ile
 225 230 235 240
 Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro Asp Asp
 245 250 255
 Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn His Lys
 260 265 270
 Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn
 275 280

<210> 4
 <211> 238

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Leu Asn Glu His Ser Met Gln Ala Leu Ser Trp Arg Lys Leu
1 5 10 15
Tyr Leu Ser Arg Ala Lys Leu Lys Ala Ser Ser Arg Thr Ser Ala Leu
20 25 30
Leu Ser Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Asp Ala
35 40 45
Asp His Asp Tyr Pro Pro Gly Leu Leu Ile Ala Phe Ser Ala Cys Thr
50 55 60
Thr Val Leu Val Ala Val His Leu Phe Ala Leu Met Ile Ser Thr Cys
65 70 75 80
Ile Leu Pro Asn Ile Glu Ala Val Ser Asn Val His Asn Leu Asn Ser
85 90 95
Val Lys Glu Ser Pro His Glu Arg Met His Arg His Ile Glu Leu Ala
100 105 110
Trp Ala Phe Ser Thr Val Ile Gly Thr Leu Leu Phe Leu Ala Glu Val
115 120 125
Val Leu Leu Cys Trp Val Lys Phe Leu Pro Leu Lys Lys Gln Pro Gly
130 135 140
Gln Pro Arg Pro Thr Ser Lys Pro Pro Ala Ser Gly Ala Ala Ala Asn
145 150 155 160
Val Ser Thr Ser Gly Ile Thr Pro Gly Gln Ala Ala Ala Ile Ala Ser
165 170 175
Thr Thr Ile Met Val Pro Phe Gly Leu Ile Phe Ile Val Phe Ala Val
180 185 190
His Phe Tyr Arg Ser Leu Val Ser His Lys Thr Asp Arg Gln Phe Gln
195 200 205
Glu Leu Asn Glu Leu Ala Glu Phe Ala Arg Leu Gln Asp Gln Leu Asp
210 215 220
His Arg Gly Asp His Pro Leu Thr Pro Gly Ser His Tyr Ala
225 230 235
5

<210> 5
 <211> 372
 <212> PRT
 <213> Homo sapiens

<400> 5

Met	Leu	Ala	Asn	Ser	Ser	Ser	Thr	Asn	Ser	Ser	Val	Leu	Pro	Cys	Pro
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Asp	Tyr	Arg	Pro	Thr	His	Arg	Leu	His	Leu	Val	Val	Tyr	Ser	Leu	Val
			20					25					30		
Leu	Ala	Ala	Gly	Leu	Pro	Leu	Asn	Ala	Leu	Ala	Leu	Trp	Val	Phe	Leu
			35					40					45		
Arg	Ala	Leu	Arg	Val	His	Ser	Val	Val	Ser	Val	Tyr	Met	Cys	Asn	Leu
		50				55					60				
Ala	Ala	Ser	Asp	Leu	Leu	Phe	Thr	Leu	Ser	Leu	Pro	Val	Arg	Leu	Ser
65				70					75					80	
Tyr	Tyr	Ala	Leu	His	His	Trp	Pro	Phe	Pro	Asp	Leu	Leu	Cys	Gln	Thr
				85					90					95	
Thr	Gly	Ala	Ile	Phe	Gln	Met	Asn	Met	Tyr	Gly	Ser	Cys	Ile	Phe	Leu
			100					105					110		
Met	Leu	Ile	Asn	Val	Asp	Arg	Tyr	Ala	Ala	Ile	Val	His	Pro	Leu	Arg
			115					120					125		
Leu	Arg	His	Leu	Arg	Arg	Pro	Arg	Val	Ala	Arg	Leu	Leu	Cys	Leu	Gly
			130					135					140		
Val	Trp	Ala	Leu	Ile	Leu	Val	Phe	Ala	Val	Pro	Ala	Ala	Arg	Val	His
145				150						155				160	
Arg	Pro	Ser	Arg	Cys	Arg	Tyr	Arg	Asp	Leu	Glu	Val	Arg	Leu	Cys	Phe
				165					170				175		
Glu	Ser	Phe	Ser	Asp	Glu	Leu	Trp	Lys	Gly	Arg	Leu	Leu	Pro	Leu	Val
				180					185				190		
Leu	Leu	Ala	Glu	Ala	Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Val	Val
			195					200					205		
Tyr	Ser	Ser	Gly	Arg	Val	Phe	Trp	Thr	Leu	Ala	Arg	Pro	Asp	Ala	Thr

210 215 220
 Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu
 225 230 235 240
 Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val
 245 250 255
 Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg
 260 265 270
 Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala
 275 280 285
 Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe
 290 295 300
 Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser
 305 310 315 320
 Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala
 325 330 335
 Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu
 340 345 350
 Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln
 355 360 365
 Asp Ser Ala Leu
 370

<210> 6
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Trp Lys Leu Trp Arg Ala Glu Glu Gly Ala Ala Ala Leu Gly Gly
 1 5 10 15
 Ala Leu Phe Leu Leu Leu Phe Ala Leu Gly Val Arg Gln Leu Leu Lys
 20 25 30
 Gln Arg Arg Pro Met Gly Phe Pro Pro Gly Pro Pro Gly Leu Pro Phe
 35 40 45
 Ile Gly Asn Ile Tyr Ser Leu Ala Ala Ser Ser Glu Leu Pro His Val

50 55 60
 Tyr Met Arg Lys Gln Ser Gln Val Tyr Gly Glu Val Gln Pro Arg Arg
 65 70 75 80
 Ala Pro Gly Arg Glu Gly Arg Gln Ala Gly Pro Gly Trp Pro Gly Pro
 85 90 95
 Ser Trp Leu Asp Leu Trp Pro Pro Leu Gly Arg Leu Val Gly Thr Ser
 100 105 110
 Pro Cys Ala Gly Cys Pro Leu Arg Asp Thr Arg Phe Pro Gly Leu Glu
 115 120 125
 Gly Arg Ser Pro Arg Arg Arg Ala Pro Leu Gln Gly Glu Pro Arg Pro
 130 135 140
 Cys Arg
 145

<210> 7
 <211> 302
 <212> PRT
 <213> Homo sapiens

<400> 7
 Met Lys Ala Pro Gly Arg Leu Val Leu Ile Ile Leu Cys Ser Val Val
 1 5 10 15
 Phe Ser Ala Val Tyr Ile Leu Leu Cys Cys Trp Ala Gly Leu Pro Leu
 20 25 30
 Cys Leu Ala Thr Cys Leu Asp His His Phe Pro Thr Gly Ser Arg Pro
 35 40 45
 Thr Val Pro Gly Pro Leu His Phe Ser Gly Tyr Ser Ser Val Pro Asp
 50 55 60
 Gly Lys Pro Leu Val Arg Glu Pro Cys Arg Ser Cys Ala Val Val Ser
 65 70 75 80
 Ser Ser Gly Gln Met Leu Gly Ser Gly Leu Gly Ala Glu Ile Asp Ser
 85 90 95
 Ala Glu Cys Val Phe Arg Met Asn Gln Ala Pro Thr Val Gly Phe Glu
 100 105 110

Ala Asp Val Gly Gln Arg Ser Thr Leu Arg Val Val Ser His Thr Ser
115 120 125
Val Pro Leu Leu Leu Arg Asn Tyr Ser His Tyr Phe Gln Lys Ala Arg
130 135 140
Asp Thr Leu Tyr Met Val Trp Gly Gln Gly Arg His Met Asp Arg Val
145 150 155 160
Leu Gly Gly Arg Thr Tyr Arg Thr Leu Leu Gln Leu Thr Arg Met Tyr
165 170 175
Pro Gly Leu Gln Val Tyr Thr Phe Thr Glu Arg Met Met Ala Tyr Cys
180 185 190
Asp Gln Ile Phe Gln Asp Glu Thr Gly Lys Asn Arg Arg Gln Ser Gly
195 200 205
Ser Phe Leu Ser Thr Gly Trp Phe Thr Met Ile Leu Ala Leu Glu Leu
210 215 220
Cys Glu Glu Ile Val Val Tyr Gly Met Val Ser Asp Ser Tyr Cys Arg
225 230 235 240
Glu Lys Ser His Pro Ser Val Pro Tyr His Tyr Phe Glu Lys Gly Arg
245 250 255
Leu Asp Glu Cys Gln Met Tyr Leu Ala His Glu Gln Ala Pro Arg Ser
260 265 270
Ala His Arg Phe Ile Thr Glu Lys Ala Val Phe Ser Arg Trp Ala Lys
275 280 285
Lys Arg Pro Ile Val Phe Ala His Pro Ser Trp Arg Thr Glu
290 295 300

<210> 8
<211> 194
<212> PRT
<213> Homo sapiens

<400> 8

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp Leu
1 5 10 15
Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser Leu Asp
20 25 30

Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu Asn Tyr
 35 40 45
 Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met Pro Tyr
 50 55 60
 Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys Tyr Cys
 65 70 75 80
 Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser Pro Gly
 85 90 95
 Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val Gln Asp
 100 105 110
 Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln Val Ser
 115 120 125
 Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln Arg Arg
 130 135 140
 Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala
 145 150 155 160
 Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys
 165 170 175
 Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His
 180 185 190
 Gly Phe

<210> 9
 <211> 542
 <212> PRT
 <213> Homo sapiens

<400> 9

Met Lys Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe
 1 5 10 15
 Leu Ser Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser
 20 25 30
 Tyr Ser Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn
 35 40 45
 Trp Ala Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser
 10

50	55	60
Val Asn Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn		
65	70	75
Ile Val Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His		
85	90	95
Asn Thr Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr		
100	105	110
Thr Glu Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg		
115	120	125
Lys Leu Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr		
130	135	140
Leu Gly Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro		
145	150	155
Arg Gln Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu		
165	170	175
Gln Glu Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala		
180	185	190
Arg Ala Gln Cys Val Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu		
195	200	205
Lys Ala Cys Gln Met Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg		
210	215	220
Cys Asn Tyr Thr Ser Val Val Met Ser Phe Ser Ile Leu Met Ser Ser		
225	230	235
Lys Ser Met Thr Asp Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu		
245	250	255
Ser Val Ser Ile Leu Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr		
260	265	270
Val Trp Ser Arg Val Val Val Thr Glu Ile Ser Tyr Met Arg His Val		
275	280	285
Cys Ile Val Asn Ile Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe		
290	295	300
Ile Ile Gly Ser His Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys		

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305          310          315          320
Val Ala Val Thr Phe Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe
          325          330          335
Trp Met Leu Phe Lys Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile
          340          345          350
Phe Arg Arg Met Met Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile
          355          360          365
Gly Tyr Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr
          370          375          380
Glu Pro Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp
385          390          395          400
Asp Asn Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile
          405          410          415
Val Ala Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln
          420          425          430
Arg Pro Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met
          435          440          445
Arg Ile Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr
          450          455          460
Trp Gly Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe
465          470          475          480
His Ile Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu
          485          490          495
Leu Phe Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met
          500          505          510
Arg Met Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser
          515          520          525
Leu Gly Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly
          530          535          540

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<210> 10
<211> 276
<212> PRT

<213> Homo sapiens

<400> 10

Met Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu
1 5 10 15
Leu Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro
20 25 30
Tyr Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala
35 40 45
Thr Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala
50 55 60
Ser Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser
65 70 75 80
Arg Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro
85 90 95
Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp
100 105 110
Gln Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val
115 120 125
Leu Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn
130 135 140
Ala Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met
145 150 155 160
Asp Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile
165 170 175
Thr Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly
180 185 190
Arg Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu
195 200 205
Ala Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe
210 215 220
Ser Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly
225 230 235 240

Ser Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu
245 250 255
Ala Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro
260 265 270
Ser Leu Ser Pro
275

<210> 11
<211> 699
<212> DNA
<213> Homo sapiens

<400> 11

atgtggcagc ttttagcagc agcatgctgg atgcttcttc ttggatctat gtatggttat	60
gacaagaaag gaaacaatgc aaaccctgaa gctaatatga atattagcca gattatttct	120
tactgggggtt atccttatga agagtatgat gttacaacaa aagatgggta tacccttgga	180
atztatagga ttccacatgg aagaggatgc ccaggaggga cagctccaaa gcctgctgtg	240
tatttgcagc atggcttaat tgcattctgcc agtaactgga ttgcaacct gcccaacaac	300
agtttggctt tccttctggc agatagtggg tatgacgtgt ggttggggaa cagccgagga	360
aacacttggg ccagaaaaca ccttaaattg tcaccgaaat caccagaata ctgggccttc	420
agtttggatg agatggctaa atatgacctt ccagccacaa tcaattttat catagagaaa	480
actggacaga agcgactcta ctacgtgggc cactcacaag gcaccacat agcttttata	540
gcattttcta caaaccaga actggctaaa aagattaaga tattttttgc actggctcca	600
gttgtcacag ttaaatacac ccaaagtcct atgaaaaaac taacaaccct ttccaggcga	660
gtagttaagg tatgtgactt cccaagtttt aatctgaaa	699

<210> 12
<211> 819
<212> DNA
<213> Homo sapiens

<400> 12

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gagcacgcct accggcccgg ccgtagggtg tgtgctgtcc gggctcacgg ggaccctgtc	120
tccgagtcgt tcgtgcagcg tgtgtaccag cccttcctca ccacctgcga cgggcaccgg	180
gcctgcagca cctaccgaac catctatagg accgcctacc gccgcagccc tgggctggcc	240
cctgccaggc ctcgctacgc gtgctgcccc ggctggaaga ggaccagcgg gcttcctggg	300
gcctgtggag cagcaatatg ccagccgcca tgccggaacg gagggagctg tgtccagcct	360

ggccgctgcc gctgccctgc aggatggcgg ggtgacctt gccagtcaga tgtggatgaa	420
tgcagtgcta ggaggggagg ctgtccccag cgctgctca acaccgccgg cagttactgg	480
tgccagtgtt gggaggggca cagcctgtct gcagacggta cactctgtgt gcccaaggga	540
gggcccccca ggggtggccc caacccgaca ggagtggaca gtgcaatgaa ggaagaagtg	600
cagaggctgc agtccagggt ggacctgctg gaggagaagc tgcagctggg gctggcccca	660
ctgcacagcc tggcctcgca ggcactggag catgggctcc cggaccccg cagcctcctg	720
gtgcactcct tccagcagct cggccgcctc gactccctga gcgagcagat ttccttcctg	780
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<210> 13
 <211> 846
 <212> DNA
 <213> Homo sapiens

<400> 13	
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attattcgag acagccctgt tctccctgtc accctgcagt gtaacctcac ctccagctct	180
cacaccctta catacagcta ctggacaaag aatgggggtg aactgagtgc cactcgtaag	240
aatgccagca acatggagta caggatcaat aagccgagag ctgaggattc aggccaatac	300
cactgcgtat atcactttgt cagcgtctct aaagcaaacg ccaccattga agtgaaagcc	360
gctcctgaca tcaactggcca taaacggagt gagaacaaga atgaagggca ggatgccact	420
atgtattgca agtcagttgg ctacccccac ccagactgga tatggcgcaa gaaggagaac	480
gggatgcccc tggacattgt caatacctct ggccgcttct tcatcatcaa caaggaaaat	540
tacactgagt tgaacattgt gaacctgcag atcacggaag accctggcga gtatgaatgt	600
aatgccacca acgccattgg ctccgcctct gttgtcactg tcctcagggt gcggagccac	660
ctggccccac tctggccttt cttgggaatt ctggctgaaa ttatcatcct tgtggtgatc	720
attgtttgtg atgagaagag gaagaggcca gatgagggtc ctgacgatga tgaaccagct	780
ggaccaatga aaaccaactc taccaacaat cacaagata aaaacttgcg ccagagaaac	840
acaaat	846

<210> 14
 <211> 714
 <212> DNA
 <213> Homo sapiens

<400> 14	
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atggtggagg tgcagctgga cgctgaccac gactaccac cggggctgct catcgcttc	180
agtgcctgca ccacagtgct ggtggctgtg cacctgtttg cgctcatgat cagcacctgc	240
atcctgcccc acatcgaggc ggtgagcaac gtgcacaatc tcaactcggc caaggagtcc	300
ccccatgagc gcatgcaccg ccacatcgag ctggcctggg ctttctccac cgtcatcggc	360
acgctgctct tcctagctga ggtggtgctg ctctgctggg tcaagttctt gcccctcaag	420
aagcagccag gccagccaag gccaccagc aagcccccg ccagtggcgc agcagccaac	480
gtcagcacca gcggcatcac cccgggccag gcagctgcca tcgcctcgac caccatcatg	540
gtgcccttcg gcctgatctt tatcgtcttc gccgtccact tctaccgctc actggttagc	600
cataagaccg accgacagtt ccaggagctc aacgagctgg cggagtttgc ccgcttacag	660
gaccagctgg accacagagg ggaccacccc ctgacgcccc gcagccacta tgcc	714

<210> 15

<211> 1116

<212> DNA

<213> Homo sapiens

<400> 15

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acccaccgcc tgcacttggt ggtctacagc ttggtgctgg ctgccgggt cccctcaac	120
gcgctagccc tctgggtctt cctgcgcgcg ctgcgcgtgc actcgggtggt gagcgtgtac	180
atgtgtaacc tggcggccag cgacctgctc ttcaccctct cgctgcccgt tcgtctctcc	240
tactacgcac tgcaccactg gcccttcccc gacctctgt gccagacgac gggcgccatc	300
ttccagatga acatgtacgg cagctgcac ttcctgatgc tcatcaacgt ggaccgctac	360
gccgccatcg tgcaccgct gcgactgcgc cacctgcggc ggccccgcgt ggcgcggctg	420
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cggagcaagc tgggtggcgg cagcgtgcct gccgcgatc gcgtgcgcgg ggtgctgatg	840
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gccgagggct tccgcaacac cctgcgcggc ctgggcactc cgcaccgggc caggacctcg	960
gccaccaacg ggacgcgggc ggcgctcgc caatccgaaa ggtccgccgt caccaccgac	1020

gccaccaggc cggatgccgc cagtcagggg ctgctccgac cctccgactc ccactctctg 1080
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<210> 16
<211> 438
<212> DNA
<213> Homo sapiens

<400> 16
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ccggggccgc cggggctgcc atttatcggc aacatctatt ccctggcagc ctcattccgag 180
cttccccatg tctacatgag aaagcagagc caggtgtacg gagaggtaca gccccgacgg 240
gccccgggca gggagggccg ccaggctggc ccgggctggc cagggccttc ctggttggac 300
ttatggccgc ccctggggcg actagtcggg acctctccgt gtgccggctg ccctttgagg 360
gacacccgct tcccgggtct ggaagggaga agtcctcgac gccgtgcccc cttgcagggg 420
gagccccgcc cctgccgg 438

<210> 17
<211> 906
<212> DNA
<213> Homo sapiens

<400> 17
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cacttcccca caggctccag gccactgtg ccgggacccc tgcacttcag tggatatagc 180
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gcgctggagc tgtgtgagga gatcgtggtc tatgggatgg tcagcgacag ctactgcagg 720
gagaagagcc acccctcagt gccttaccac tactttgaga agggccggct agatgagtgt 780
cagatgtacc tggcacacga gcaggcgccc cgaagcgccc accgcttcat cactgagaag 840

gcggtcttct cccgctgggc caagaagagg cccatcgtgt tcgcccattcc gtcctggagg	900
actgag	906

<210> 18
 <211> 582
 <212> DNA
 <213> Homo sapiens

<400> 18

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aactggggat gctatggaaa catccaaagc ctggacaccc ctggagcatc ttgtgggatt	120
ggaagacgtc acggcctgaa ctactgtgga gttcgtgctt ctgaaaggct ggctgaaata	180
gacatgccat acctcctgaa atatcaaccc atgatgcaaa ccattggcca aaagtactgc	240
atggatcctg ccgtgatcgc tgggtgtcttg tccaggaagt ctcccggatga caaaattctg	300
gtcaacatgg gcgataggac tagcatgggtg caggaccctg gctctcaagc tcccacatcc	360
tggattagtg agtctcaggt ttcccagaca actgaagttc tgactactag aatcaaagaa	420
atccagagga ggtttccaac ctggaccctt gaccagtacc tgagaggtgg actctgtgcc	480
tacagtgggg gtgctggcta tgtccgaagc agccaggacc tgagctgtga cttctgcaat	540
gatgtccttg cacgagccaa gtacctcaag agacatggct tc	582

<210> 19
 <211> 1626
 <212> DNA
 <213> Homo sapiens

<400> 19

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ctcgacacag cagccatttc aaactgggct ttcatccca acaaaaatgc cagctcggat	180
ttgttgacgt cagtgaattt gtttgccaga caactccaca tccacaataa ttctgagaac	240
attgtgaatg aactcttcat tcagacaaaa gggtttcaca tcaaccataa tacctcagag	300
aaaagcctca atttctccat gagcatgaac aataccacag aagatatctt aggaatggta	360
cagattccca ggcaagagct aaggaagctg tggccaaatg catcccaagc cattagcata	420
gctttcccaa ccttgggggc taccctgaga gaagccact tgcaaaatgt gagtcttccc	480
agacaggtaa atggtctggt gctatcagtg gttttaccag aaagggtgca agaaatcata	540
ctcaccttcg aaaagatcaa taaaacccgc aatgccagag ccagtggtg ttgctggcac	600
tccaagaaaa ggagatggga tgagaaagcg tgccaaatga tgttgatata caggaacgaa	660
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aaatcgatga ccgacaaagt tctggactac atcacctgca ttgggctcag cgtctcaatc	780
ctaagcttgg ttctttgcct gatcattgaa gccacagtgt ggtcccgggt ggttgtagcg	840
gagatatcat acatgctga cgtgtgcatc gtgaatatag cagtgtccct tctgactgcc	900
aatgtgtggt ttatcatagg ctctcacttt aacattaagg cccaggacta caacatgtgt	960
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atgatggtca ttggctttgc cattggctat gggtgcccat tgatcattgc tgtcactaca	1140
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attatggatc acaagataag agatgctttg aggatgagga tgtcttcact gaaggggaaa	1560
tcgagggcag ctgagaatgc atcactaggc ccaaccaatg gatctaaatt aatgaatcgt	1620
caagga	1626

<210> 20
 <211> 828
 <212> DNA
 <213> Homo sapiens

<400> 20

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tgtctccggc ccagcctgag cctggagctg gtgccctaca caccacagat aacagcttgg	120
gacctggaag ggaaggtcac agccaccacc ttctccctgg agcagccgag ctgtgtcttc	180
gatgggcttg ccagcgccag cgataccgtc tggctcgtgg tggccttcag caatgcctcc	240
aggggcttcc agaaccgga gacactggct gacattccgg cctccccaca gctgctgacc	300
gatggccact acatgacgct gccctgtct cgggaccagc tgccctgtgg cgaccccatg	360
gcgggcagcg gaggcgcccc cgtgctgcgg gtgggcatg accacggctg ccaccagcag	420
cccttctgca acgcgccct ccctggccct ggaccctatc gggatgaagt cctcctgatg	480
gacaccaggg gctcaccag ggctgagacc aagtggtcag accccatcac tctccaccaa	540
gggaagaccc ccgatccat cgacacctgg ccagggcggc gaagtggcag catgatcgtc	600
attacctcca tcctctcttc tctggccggc ctctactct tggccttctt ggcagcctct	660

accatgcgct tctccagcct gtggtggccg gaggaggccc cggagcagct gcggatcggc	720
tccttcatgg gcaagcgcta catgaccac cacatcccac ccagcgaggc cgccacactg	780
ccggtgggct gcaagcctgg cctggacccc ctccccagcc tcagcccc	828

<210> 21
 <211> 1308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)...(777)

<400> 21

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taaggcagat cccaa atg tgg cag ctt tta gca gca gca tgc tgg atg ctt	111

Met Trp Gln Leu Leu Ala Ala Ala Cys Trp Met Leu

1 5 10

ctt ctt gga tct atg tat ggt tat gac aag aaa gga aac aat gca aac	159
Leu Leu Gly Ser Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn	

15 20 25

cct gaa gct aat atg aat att agc cag att att tct tac tgg ggt tat	207
Pro Glu Ala Asn Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr	

30 35 40

cct tat gaa gag tat gat gtt aca aca aaa gat ggt tat atc ctt gga	255
Pro Tyr Glu Glu Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly	

45 50 55 60

att tat agg att cca cat gga aga gga tgc cca ggg agg aca gct cca	303
Ile Tyr Arg Ile Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro	

65 70 75

aag cct gct gtg tat ttg cag cat ggc tta att gca tct gcc agt aac	351
Lys Pro Ala Val Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn	

80 85 90

tgg att tgc aac ctg ccc aac aac agt ttg gct ttc ctt ctg gca gat	399
Trp Ile Cys Asn Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp	

95 100 105

agt ggt tat gac gtg tgg ttg ggg aac agc cga gga aac act tgg tcc	447
Ser Gly Tyr Asp Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser	

+

-

110	115	120	
aga aaa cac ctt aaa ttg tca ccg aaa tca cca gaa tac tgg gcc ttc			495
Arg Lys His Leu Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe			
125	130	135	140
agt ttg gat gag atg gct aaa tat gac ctt cca gcc aca atc aat ttt			543
Ser Leu Asp Glu Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe			
145	150	155	
atc ata gag aaa act gga cag aag cga ctc tac tac gtg ggc cac tca			591
Ile Ile Glu Lys Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser			
160	165	170	
caa ggc acc acc ata gct ttt ata gca ttt tct aca aac cca gaa ctg			639
Gln Gly Thr Thr Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu			
175	180	185	
gct aaa aag att aag ata ttt ttt gca ctg gct cca gtt gtc aca gtt			687
Ala Lys Lys Ile Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val			
190	195	200	
aaa tac acc caa agt cct atg aaa aaa cta aca acc ctt tcc agg cga			735
Lys Tyr Thr Gln Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg			
205	210	215	220
gta gtt aag gta tgt gac ttc cca agt ttt aat ctg aaa taacta			780
Val Val Lys Val Cys Asp Phe Pro Ser Phe Asn Leu Lys			
225	230		
aaagtagctc tatttccatt gatttcaaca gaagaccaat gacattttac aaacttctga			840
gaaaataata ggtattcaag atatccatgt aagttcactg atgatgtatg caatcttatt			900
agcagagtgc agggaaactcc ccctgttgct aatctgccct actttcttca tctatgtcta			960
gaaacgtgtc tgctgcgcca ttcctcaacc acagatagag agaacttatt tgattgattg			1020
gtttgttgaa tttagtagat tgaatttttc tagtgatccc taatttttta ggggcagtgg			1080
tggttgagtt cacagcatgg aatcagatgg tgtgtgtttg aatgttattt ctatgatttg			1140
caagctgggt aaatttggtc aagaccttaa gttctcttca tctgtaatgt ggggataata			1200
atagttctta ctcatagggc taccctgagg actaagtaaa ttaatacagc atatcctcta			1260
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<210> 22
 <211> 1272
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)...(881)

<400> 22

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atg agg ggc tct cag gag gtg ctg ctg atg tgg ctt ctg gtg ttg gca	107
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala	
1 5 10 15	
gtg ggc ggc aca gag cac gcc tac cgg ccc ggc cgt agg gtg tgt gct	155
Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala	
20 25 30	
gtc cgg gct cac ggg gac cct gtc tcc gag tcg ttc gtg cag cgt gtg	203
Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val	
35 40 45	
tac cag ccc ttc ctc acc acc tgc gac ggg cac cgg gcc tgc agc acc	251
Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr	
50 55 60	
tac cga acc atc tat agg acc gcc tac cgc cgc agc cct ggg ctg gcc	299
Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala	
65 70 75 80	
cct gcc agg cct cgc tac gcg tgc tgc ccc ggc tgg aag agg acc agc	347
Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser	
85 90 95	
ggg ctt cct ggg gcc tgt gga gca gca ata tgc cag ccg cca tgc cgg	395
Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg	
100 105 110	
aac gga ggg agc tgt gtc cag cct ggc cgc tgc cgc tgc cct gca gga	443
Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly	
115 120 125	
tgg cgg ggt gac act tgc cag tca gat gtg gat gaa tgc agt gct agg	491
Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg	

130	135	140	
agg ggc ggc tgt ccc cag cgc tgc gtc aac acc gcc ggc agt tac tgg			539
Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp			
145	150	155	160
tgc cag tgt tgg gag ggg cac agc ctg tct gca gac ggt aca ctc tgt			587
Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys			
165	170	175	
gtg ccc aag gga ggg ccc ccc agg gtg gcc ccc aac ccg aca gga gtg			635
Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val			
180	185	190	
gac agt gca atg aag gaa gaa gtg cag agg ctg cag tcc agg gtg gac			683
Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp			
195	200	205	
ctg ctg gag gag aag ctg cag ctg gtg ctg gcc cca ctg cac agc ctg			731
Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu			
210	215	220	
gcc tcg cag gca ctg gag cat ggg ctc ccg gac ccc ggc agc ctc ctg			779
Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu			
225	230	235	240
gtg cac tcc ttc cag cag ctc ggc cgc atc gac tcc ctg agc gag cag			827
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln			
245	250	255	
att tcc ttc ctg gag gag cag ctg ggg tcc tgc tcc tgc aag aaa gac			875
Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp			
260	265	270	
tcg tgactgccca gcgccccagg ctggactgag cccctcacgc cgccctgcag cc			930
Ser			
cccatgcccc tgcccaacat gctgggggtc cagaagccac ctcgggggtga ctgagcggaa			990
ggccaggcag ggccttcctc ctcttcctcc tccccttcct cgggaggctc cccagaccct			1050
ggcatgggat gggctgggat cttctctgtg aatccacccc tggctacccc caccctggct			1110
acccaacgg catccaagg ccagggtgggc cctcagctga gggaaggtac gagctccctg			1170
ctggagcctg ggacccatgg cacaggccag gcagcccgga ggctgggtgg ggcctcagt			1230

ggggctgctg cctgaccccc agcacaataa aaatgaaacg tg

1272

<210> 23
<211> 2083
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (188)...(1036)

<400> 23

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tcccctccct tccccggccc cggctctggc cccggcccat tcgctgttgg gtcttctgct 180

agggagg atg tcg ggt tcg tcg ctg ccc agc gcc ctg gcc ctc tcg ctg 229

Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu

1 5 10

ttg ctg gtc tct ggc tcc ctc ctc cca ggg cca ggc gcc gct cag aac 277

Leu Leu Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn

15 20 25 30

gag cca agg att gtc acc agt gaa gag gtc att att cga gac agc cct 325

Glu Pro Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro

35 40 45

gtt ctc cct gtc acc ctg cag tgt aac ctc acc tcc agc tct cac acc 373

Val Leu Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr

50 55 60

ctt aca tac agc tac tgg aca aag aat ggg gtg gaa ctg agt gcc act 421

Leu Thr Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr

65 70 75

cgt aag aat gcc agc aac atg gag tac agg atc aat aag ccg aga gct 469

Arg Lys Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala

80 85 90

gag gat tca ggc gaa tac cac tgc gta tat cac ttt gtc agc gct cct 517

Glu Asp Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro

95 100 105 110

aaa gca aac gcc acc att gaa gtg aaa gcc gct cct gac atc act ggc 565

Lys Ala Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly	
115 120 125	
cat aaa cgg agt gag aac aag aat gaa ggg cag gat gcc act atg tat	613
His Lys Arg Ser Glu Asn Lys Asn Glu Gly Gln Asp Ala Thr Met Tyr	
130 135 140	
tgc aag tca gtt ggc tac ccc cac cca gac tgg ata tgg cgc aag aag	661
Cys Lys Ser Val Gly Tyr Pro His Pro Asp Trp Ile Trp Arg Lys Lys	
145 150 155	
gag aac ggg atg ccc atg gac att gtc aat acc tct ggc cgc ttc ttc	709
Glu Asn Gly Met Pro Met Asp Ile Val Asn Thr Ser Gly Arg Phe Phe	
160 165 170	
atc atc aac aag gaa aat tac act gag ttg aac att gtg aac ctg cag	757
Ile Ile Asn Lys Glu Asn Tyr Thr Glu Leu Asn Ile Val Asn Leu Gln	
175 180 185 190	
atc acg gaa gac cct ggc gag tat gaa tgt aat gcc acc aac gcc att	805
Ile Thr Glu Asp Pro Gly Glu Tyr Glu Cys Asn Ala Thr Asn Ala Ile	
195 200 205	
ggc tcc gcc tct gtt gtc act gtc ctc agg gtg cgg agc cac ctg gcc	853
Gly Ser Ala Ser Val Val Thr Val Leu Arg Val Arg Ser His Leu Ala	
210 215 220	
cca ctc tgg cct ttc ttg gga att ctg gct gaa att atc atc ctt gtg	901
Pro Leu Trp Pro Phe Leu Gly Ile Leu Ala Glu Ile Ile Ile Leu Val	
225 230 235	
gtg atc att gtt gtg tat gag aag agg aag agg cca gat gag gtt cct	949
Val Ile Ile Val Val Tyr Glu Lys Arg Lys Arg Pro Asp Glu Val Pro	
240 245 250	
gac gat gat gaa cca gct gga cca atg aaa acc aac tct acc aac aat	997
Asp Asp Asp Glu Pro Ala Gly Pro Met Lys Thr Asn Ser Thr Asn Asn	
255 260 265 270	
cac aaa gat aaa aac ttg cgc cag aga aac aca aat taagtac	1040
His Lys Asp Lys Asn Leu Arg Gln Arg Asn Thr Asn	
275 280	

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tgcttacaat atcttttaggt tcctgaaact ggtggcaaca tgacctgcta aaatcttctg 1100
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acctgtgact ttaataagct ggaacagtc actgaatggg tataatgaat tgcagtatat 1700
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ttataatctt tcttttggtt ccaatgacct tgaaatgtta tagcatggta atattctatg 1880
caactatagt tatacttttt gggttgacac tgtatttttt cacattgatt tactgggtga 1940
tgatagatct tataacctaa cggttctcat gcggtgcgta attgtagatg catgtacttg 2000
tgtgttttgt gtaattattg aagtgcagt atgtataaaa aagtggattc acctgttttt 2060
aaaaataaaa cattgataaa agg 2083

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<210> 24
<211> 1260
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (147)...(863)

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<400> 24

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gggacgggga gccccgggg gccccgccac tgccgccgtc cgccgtcacc taccgggact 120
ggatcggcca gagttactcc gaggtg atg agc ctc aac gag cac tcc atg 170

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Met Ser Leu Asn Glu His Ser Met

1 5

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cag gcg ctg tcc tgg cgc aag ctc tac ttg agc cgc gcc aag ctt aaa 218
Gln Ala Leu Ser Trp Arg Lys Leu Tyr Leu Ser Arg Ala Lys Leu Lys

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10	15	20	
gcc tcc agc cgg acc tcg gct ctg ctc tcc ggc ttc gcc atg gtg gca	266		
Ala Ser Ser Arg Thr Ser Ala Leu Leu Ser Gly Phe Ala Met Val Ala			
25	30	35	40
atg gtg gag gtg cag ctg gac gct gac cac gac tac cca ccg ggg ctg	314		
Met Val Glu Val Gln Leu Asp Ala Asp His Asp Tyr Pro Pro Gly Leu			
45	50	55	
ctc atc gcc ttc agt gcc tgc acc aca gtg ctg gtg gct gtg cac ctg	362		
Leu Ile Ala Phe Ser Ala Cys Thr Thr Val Leu Val Ala Val His Leu			
60	65	70	
ttt gcg ctc atg atc agc acc tgc atc ctg ccc aac atc gag gcg gtg	410		
Phe Ala Leu Met Ile Ser Thr Cys Ile Leu Pro Asn Ile Glu Ala Val			
75	80	85	
agc aac gtg cac aat ctc aac tcg gtc aag gag tcc ccc cat gag cgc	458		
Ser Asn Val His Asn Leu Asn Ser Val Lys Glu Ser Pro His Glu Arg			
90	95	100	
atg cac cgc cac atc gag ctg gcc tgg gcc ttc tcc acc gtc atc ggc	506		
Met His Arg His Ile Glu Leu Ala Trp Ala Phe Ser Thr Val Ile Gly			
105	110	115	120
acg ctg ctc ttc cta gct gag gtg gtg ctg ctc tgc tgg gtc aag ttc	554		
Thr Leu Leu Phe Leu Ala Glu Val Val Leu Leu Cys Trp Val Lys Phe			
125	130	135	
ttg ccc ctc aag aag cag cca ggc cag cca agg ccc acc agc aag ccc	602		
Leu Pro Leu Lys Lys Gln Pro Gly Gln Pro Arg Pro Thr Ser Lys Pro			
140	145	150	
ccc gcc agt ggc gca gca gcc aac gtc agc acc agc ggc atc acc ccg	650		
Pro Ala Ser Gly Ala Ala Ala Asn Val Ser Thr Ser Gly Ile Thr Pro			
155	160	165	
ggc cag gca gct gcc atc gcc tcg acc acc atc atg gtg ccc ttc ggc	698		
Gly Gln Ala Ala Ala Ile Ala Ser Thr Thr Ile Met Val Pro Phe Gly			
170	175	180	
ctg atc ttt atc gtc ttc gcc gtc cac ttc tac cgc tca ctg gtt agc	746		

Leu Ile Phe Ile Val	Phe Ala Val His Phe Tyr Arg Ser Leu Val Ser		
185	190	195	200
cat aag acc gac cga cag ttc cag gag ctc aac gag ctg gcg gag ttt			794
His Lys Thr Asp Arg Gln Phe Gln Glu Leu Asn Glu Leu Ala Glu Phe			
205	210	215	
gcc cgc tta cag gac cag ctg gac cac aga ggg gac cac ccc ctg acg			842
Ala Arg Leu Gln Asp Gln Leu Asp His Arg Gly Asp His Pro Leu Thr			
220	225	230	
ccc gcc agc cac tat gcc taggcccatg tggtctgggc ccttccagtg			890
Pro Gly Ser His Tyr Ala			
235			
ctttggcctt acgcccttcc ccttgacctt gtcctgcccc agcctcacgg acagcctgcg			950
cagggggctg ggcttcagca aggggcagag cgtggaggga agaggatttt tataagagaa			1010
atctctgcac ttgaaactg tcctctaaga gaataagcat ttcctgttct tccagctcca			1070
ggtccacctc ctgttgaggag gcggtggggg gccaaagtgg ggccacacac tcgctgtgtc			1130
ccctctctc ccctgtgcc gtgccacctg ggtgcctcct cctgtcctgt ccgtctcaac			1190
ctccctcccg tccagcattg agtgtgtaca tgtgtgtgtg acacataaat atactcataa			1250
ggacacctcc			1260

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<210> 25
<211> 1720
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (282)...(1400)
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<400> 25

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aggagggtctc tgctgctgat gaagctgtga ccaaacgcac ccaacccttg gcagccatct	120
gtccctgcag ccatagccca cattcccatg acctccctct gcttgttttg ggaccatgtc	180
tgtacagcct ctaggccccca gccccggagg tgaatgccat gccatgattc tgggtgtgctc	240
catggcatcc ccagcctagc tcccaatccc actttggcac g atg tta gcc aac	293

Met Leu Ala Asn

1

agc tcc tca acc aac agt tct gtt ctc ccg tgt cct gac tac cga cct 341

Ser	Ser	Ser	Thr	Asn	Ser	Ser	Val	Leu	Pro	Cys	Pro	Asp	Tyr	Arg	Pro	
5					10					15					20	
acc	cac	cgc	ctg	cac	ttg	gtg	gtc	tac	agc	ttg	gtg	ctg	gct	gcc	ggg	389
Thr	His	Arg	Leu	His	Leu	Val	Val	Tyr	Ser	Leu	Val	Leu	Ala	Ala	Gly	
				25					30					35		
ctc	ccc	ctc	aac	gcg	cta	gcc	ctc	tgg	gtc	ttc	ctg	cgc	gcg	ctg	cgc	437
Leu	Pro	Leu	Asn	Ala	Leu	Ala	Leu	Trp	Val	Phe	Leu	Arg	Ala	Leu	Arg	
			40					45					50			
gtg	cac	tcg	gtg	gtg	agc	gtg	tac	atg	tgt	aac	ctg	gcg	gcc	agc	gac	485
Val	His	Ser	Val	Val	Ser	Val	Tyr	Met	Cys	Asn	Leu	Ala	Ala	Ser	Asp	
		55				60					65					
ctg	ctc	ttc	acc	ctc	tcg	ctg	ccc	gtt	cgt	ctc	tcc	tac	tac	gca	ctg	533
Leu	Leu	Phe	Thr	Leu	Ser	Leu	Pro	Val	Arg	Leu	Ser	Tyr	Tyr	Ala	Leu	
	70					75				80						
cac	cac	tgg	ccc	ttc	ccc	gac	ctc	ctg	tgc	cag	acg	acg	ggc	gcc	atc	581
His	His	Trp	Pro	Phe	Pro	Asp	Leu	Leu	Cys	Gln	Thr	Thr	Gly	Ala	Ile	
	85			90					95					100		
ttc	cag	atg	aac	atg	tac	ggc	agc	tgc	atc	ttc	ctg	atg	ctc	atc	aac	629
Phe	Gln	Met	Asn	Met	Tyr	Gly	Ser	Cys	Ile	Phe	Leu	Met	Leu	Ile	Asn	
			105					110					115			
gtg	gac	cgc	tac	gcc	gcc	atc	gtg	cac	ccg	ctg	cga	ctg	cgc	cac	ctg	677
Val	Asp	Arg	Tyr	Ala	Ala	Ile	Val	His	Pro	Leu	Arg	Leu	Arg	His	Leu	
			120					125					130			
cgg	cgg	ccc	cgc	gtg	gcg	cgg	ctg	ctc	tgc	ctg	ggc	gtg	tgg	gcg	ctc	725
Arg	Arg	Pro	Arg	Val	Ala	Arg	Leu	Leu	Cys	Leu	Gly	Val	Trp	Ala	Leu	
		135				140						145				
atc	ctg	gtg	ttt	gcc	gtg	ccc	gcc	gcc	cgc	gtg	cac	agg	ccc	tcg	cgt	773
Ile	Leu	Val	Phe	Ala	Val	Pro	Ala	Ala	Arg	Val	His	Arg	Pro	Ser	Arg	
	150				155				160							
tgc	cgc	tac	cgg	gac	ctc	gag	gtg	cgc	cta	tgc	ttc	gag	agc	ttc	agc	821
Cys	Arg	Tyr	Arg	Asp	Leu	Glu	Val	Arg	Leu	Cys	Phe	Glu	Ser	Phe	Ser	
165				170					175					180		

gac gag ctg tgg aaa ggc agg ctg ctg ccc ctc gtg ctg ctg gcc gag	869
Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val Leu Leu Ala Glu	
185 190 195	
gcg ctg ggc ttc ctg ctg ccc ctg gcg gcg gtg gtc tac tcg tcg ggc	917
Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val Tyr Ser Ser Gly	
200 205 210	
cga gtc ttc tgg acg ctg gcg cgc ccc gac gcc acg cag agc cag cgg	965
Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr Gln Ser Gln Arg	
215 220 225	
cgg cgg aag acc gtg cgc ctc ctg ctg gct aac ctc gtc atc ttc ctg	1013
Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu Val Ile Phe Leu	
230 235 240	
ctg tgc ttc gtg ccc tac aac agc acg ctg gcg gtc tac ggg ctg ctg	1061
Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val Tyr Gly Leu Leu	
245 250 255 260	
cgg agc aag ctg gtg gcg gcc agc gtg cct gcc cgc gat cgc gtg cgc	1109
Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg Asp Arg Val Arg	
265 270 275	
ggg gtg ctg atg gtg atg gtg ctg ctg gcc ggc gcc aac tgc gtg ctg	1157
Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala Asn Cys Val Leu	
280 285 290	
gac ccg ctg gtg tac tac ttt agc gcc gag ggc ttc cgc aac acc ctg	1205
Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe Arg Asn Thr Leu	
295 300 305	
cgc ggc ctg ggc act ccg cac cgg gcc agg acc tcg gcc acc aac ggg	1253
Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser Ala Thr Asn Gly	
310 315 320	
acg cgg gcg gcg ctc gcg caa tcc gaa agg tcc gcc gtc acc acc gac	1301
Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala Val Thr Thr Asp	
325 330 335 340	
gcc acc agg ccg gat gcc gcc agt cag ggg ctg ctc cga ccc tcc gac	1349
Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu Arg Pro Ser Asp	

345	350	355	
tcc cac tct ctg tct tcc ttc aca cag tgt ccc cag gat tcc gcc ctc			1397
Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln Asp Ser Ala Leu			
360	365	370	
tga acacacatgc cattgcgctg tccgtgccccg actcccaacg cctctcgttc			1450
tgggaggcctt acaggggtgta cacacaagaa ggtgggctgg gcacttggac ctttgggtgg			1510
caattccagc ttagcaacgc agaagagtac aaagtgtgga agccagggcc caggggaaggc			1570
agtgtgtctg gaaatggctt ctttaaaactg tgagcacgca gagcaccctt tctccagcgg			1630
tgggaagtga tgcagagagc ccacccgtgc agagggcaga agaggacgaa atgcctttgg			1690
gtgggcaggg cattaaactg ctaaaagctg			1720

<210> 26
 <211> 2237
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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Met Trp Lys Leu Trp Arg Ala Glu Glu	
1 5	
ggc gcg gcg gcg ctc ggc ggc gcg ctc ttc ctg ctg ctc ttc gcg cta	99
Gly Ala Ala Ala Leu Gly Gly Ala Leu Phe Leu Leu Leu Phe Ala Leu	
10 15 20 25	
ggg gtc cgc cag ctg ctg aag cag agg cgg ccg atg ggc ttc ccc ccg	147
Gly Val Arg Gln Leu Leu Lys Gln Arg Arg Pro Met Gly Phe Pro Pro	
30 35 40	
ggg ccg ccg ggc ctg cca ttt atc ggc aac atc tat tcc ctg gca gcc	195
Gly Pro Pro Gly Leu Pro Phe Ile Gly Asn Ile Tyr Ser Leu Ala Ala	
45 50 55	
tca tcc gag ctt ccc cat gtc tac atg aga aag cag agc cag gtg tac	243
Ser Ser Glu Leu Pro His Val Tyr Met Arg Lys Gln Ser Gln Val Tyr	
60 65 70	

gga gag gta cag ccc cga cgg gcc ccg ggc agg gag ggc cgc cag gct	291
Gly Glu Val Gln Pro Arg Arg Ala Pro Gly Arg Glu Gly Arg Gln Ala	
75 80 85	
ggc ccg ggc tgg cca ggg cct tcc tgg ttg gac tta tgg ccg ccc ctg	339
Gly Pro Gly Trp Pro Gly Pro Ser Trp Leu Asp Leu Trp Pro Pro Leu	
90 95 100 105	
ggc cga cta gtc ggg acc tct ccg tgt gcc ggc tgc cct ttg agg gac	387
Gly Arg Leu Val Gly Thr Ser Pro Cys Ala Gly Cys Pro Leu Arg Asp	
110 115 120	
acc cgc ttc ccg ggt ctg gaa ggg aga agt cct cga cgc cgt gcc ccc	435
Thr Arg Phe Pro Gly Leu Glu Gly Arg Ser Pro Arg Arg Arg Ala Pro	
125 130 135	
ttg cag ggg gag ccc cgc ccc tgc cgg tgaccactc cgggccga	480
Leu Gln Gly Glu Pro Arg Pro Cys Arg	
140 145	
ggctccgagg cgatccagtc ctgattttcc cgctaccgct cgagctcttg ctcttgcgcc	540
tgcgccgttt ggctcgccag ccgcgccgcc acttcaggtc caggggtggac gcatgccctc	600
aggtgcgggc gtcttgcgag tcggcctcgc agctctgttg aagctgcacg cggcttgctg	660
gaaaatcaag gcgttctgag ttctagatgg ttaatagcag gttcttcggt gtctgcagtc	720
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ctgagaagcg ggccctggga aacgattgtg aacgcgtgaa tgaattgatg actaaaatcc	840
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ttaaaactca taaccagccg gtgaggtcgg tacttcgctc ctctcattc tgcggagggg	1020
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ttcagtttag atcttgagg catatcaact gtggttctaa atggctatga ttagtaaaag	1140
gaatgccttg ttcacaaag cgaaattttt gcagacagac catgccttcc tttattcatg	1200
aagatgacaa aaatgggagg cttactcaat tccagatatg gccgaggatg ggttgatcac	1260
agacgattag ctgtaaacag ttttcgatat tttggatatg gccaaaagtc ttttgaatct	1320
aaaatcttgg aagaaaccaa atttttcaat gatgctattg aaacatacaa aggtagacct	1380
tttgacttta aacagttaat aacgaatgct gtttcaaaca taaccaatct gatcattttt	1440
ggagaacgat tcacttatga agacaccgat tttcagcaca tgattgagtt atttagtgaa	1500


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aatgtggaac tagctgccag tgcctcagtc ttcttgata atgcctttcc atggattggc 1560
atcctgcctt ttggaaaaca tcaacagctg tttagaaatg cagctgtagt ctatgatttt 1620
ctctccagac tcattgaaaa agcttcagtc aacagaaagc ctcagctacc tcagcatttt 1680
gttgatgctt atttagatga gatggatcaa ggtaaaaatg acccatcatc tactttctcc 1740
aaagaaaacc taattttctc agtgggtgaa ctcatcattg ctggaactga aactacaacc 1800
aatgtgctac ggtgggcgat tcttttcattg gccctttatc ctaatattca agtactggag 1860
agaccagaa gtgttccatc ctgagcgatt tctggacagc agtggatatt ttgccaagaa 1920
ggaagctttg gttccttttt ccctaggaag aagacattgt cttggagaac acttggtctg 1980
gatggaaatg ttcttgtttt ttacagcatt gcttcagagg ttctatttgc attttccaca 2040
tgaactagtt ccagatctga agcccaggtt aggcattgaca ttgcagcccc aaccctacct 2100
catctgtgct gaaagacgct gaaactgcct gggatgtttt cggaacaag aatgtatatt 2160
tgccttatcc ctgaacttgg tttaatcaaa tcaatgtgtg tattagaata aaagtcacag 2220
catcaaaaag ccaaattg 2237

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<210> 27
<211> 1687
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (268)...(1176)

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aatctggaag ggcggtgaaa aacctacgtc ctgccctcgc ccggcctctc cattcgtccc 180
ccgggtagag aggtgcccgg ctcccacccc ttcccagccc cagccctgga gacagcagcc 240
cctagactac tgagggacag cgacagc atg aag gct ccg ggt cgg ctc gtg 291

```

Met Lys Ala Pro Gly Arg Leu Val

1 5

```

ctc atc atc ctg tgc tcc gtg gtc ttc tct gcc gtc tac atc ctc ctg 339
Leu Ile Ile Leu Cys Ser Val Val Phe Ser Ala Val Tyr Ile Leu Leu

```

10 15 20

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tgc tgc tgg gcc ggc ctg ccc ctc tgc ctg gcc acc tgc ctg gac cac 387
Cys Cys Trp Ala Gly Leu Pro Leu Cys Leu Ala Thr Cys Leu Asp His

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25 30 35 40
33

cac ttc ccc aca ggc tcc agg ccc act gtg ccg gga ccc ctg cac ttc	435
His Phe Pro Thr Gly Ser Arg Pro Thr Val Pro Gly Pro Leu His Phe	
45 50 55	
agt gga tat agc agt gtg cca gat ggg aag ccg ctg gtc cgc gag ccc	483
Ser Gly Tyr Ser Ser Val Pro Asp Gly Lys Pro Leu Val Arg Glu Pro	
60 65 70	
tgc cgc agc tgt gcc gtg gtg tcc agc tcc ggc caa atg ctg ggc tca	531
Cys Arg Ser Cys Ala Val Val Ser Ser Ser Gly Gln Met Leu Gly Ser	
75 80 85	
ggc ctg ggt gct gag atc gac agt gcc gag tgc gtg ttc cgc atg aac	579
Gly Leu Gly Ala Glu Ile Asp Ser Ala Glu Cys Val Phe Arg Met Asn	
90 95 100	
cag gcg ccc acc gtg ggc ttt gag gcg gat gtg ggc cag cgc agc acc	627
Gln Ala Pro Thr Val Gly Phe Glu Ala Asp Val Gly Gln Arg Ser Thr	
105 110 115 120	
ctg cgt gtc gtc tca cac aca agc gtg ccg ctg ctg ctg cgc aac tat	675
Leu Arg Val Val Ser His Thr Ser Val Pro Leu Leu Leu Arg Asn Tyr	
125 130 135	
tca cac tac ttc cag aag gcc cga gac acg ctc tac atg gtg tgg ggc	723
Ser His Tyr Phe Gln Lys Ala Arg Asp Thr Leu Tyr Met Val Trp Gly	
140 145 150	
cag ggc agg cac atg gac cgg gtg ctc ggc ggc cgc acc tac cgc acg	771
Gln Gly Arg His Met Asp Arg Val Leu Gly Gly Arg Thr Tyr Arg Thr	
155 160 165	
ctg ctg cag ctc acc agg atg tac ccc ggc ctg cag gtg tac acc ttc	819
Leu Leu Gln Leu Thr Arg Met Tyr Pro Gly Leu Gln Val Tyr Thr Phe	
170 175 180	
acg gag cgc atg atg gcc tac tgc gac cag atc ttc cag gac gag acg	867
Thr Glu Arg Met Met Ala Tyr Cys Asp Gln Ile Phe Gln Asp Glu Thr	
185 190 195 200	
ggc aag aac cgg agg cag tcg ggc tcc ttc ctc agc acc ggc tgg ttc	915
Gly Lys Asn Arg Arg Gln Ser Gly Ser Phe Leu Ser Thr Gly Trp Phe	

205	210	215	
acc atg atc ctc gcg ctg gag ctg tgt gag gag atc gtg gtc tat ggg			963
Thr Met Ile Leu Ala Leu Glu Leu Cys Glu Glu Ile Val Val Tyr Gly			
220	225	230	
atg gtc agc gac agc tac tgc agg gag aag agc cac ccc tca gtg cct			1011
Met Val Ser Asp Ser Tyr Cys Arg Glu Lys Ser His Pro Ser Val Pro			
235	240	245	
tac cac tac ttt gag aag ggc cgg cta gat gag tgt cag atg tac ctg			1059
Tyr His Tyr Phe Glu Lys Gly Arg Leu Asp Glu Cys Gln Met Tyr Leu			
250	255	260	
gca cac gag cag gcg ccc cga agc gcc cac cgc ttc atc act gag aag			1107
Ala His Glu Gln Ala Pro Arg Ser Ala His Arg Phe Ile Thr Glu Lys			
265	270	275	280
gcg gtc ttc tcc cgc tgg gcc aag aag agg ccc atc gtg ttc gcc cat			1155
Ala Val Phe Ser Arg Trp Ala Lys Lys Arg Pro Ile Val Phe Ala His			
285	290	295	
ccg tcc tgg agg act gag tagcttccgt cgtcctgccca gccgccatgc cgttgcg			1210
Pro Ser Trp Arg Thr Glu			
300			
aggcctccgg gatgtcccat cccaagccat cacactccac aaaaacattt aatttatgga			1270
tcctgcctcc tgccacgtgc tgggtggacc taaggttcct tcccgcccca ttctggcgac			1330
acttgagacc atctcaggcc tcatgacttg aaggggagtg gaggggggag ccgtgtctcc			1390
cccctccact ccctgagtaa ttcattggcat ttgggggctc accccacctc caggtctgtc			1450
aagtggcctt tgtccctggg gctgatggcc cccaactcac cagcatcatg acctgtgcc			1510
agtcctggtc ctccctcccc agccgcccct accacctttt ggtgccacac ttctcaggct			1570
ggccgcccctg gttggggcag ccgagagcct ggggttcatt ggtgaagggg ccttggagtt			1630
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<210> 28
 <211> 963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (246)...(830)

<400> 28

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aggactctat ataaatcgct gtgggctcac cacctctaag gaggagcact gactgaagac 120
agaaaaattg atgaactgaa gaagacatgg tccattatgc cttacaaact tacacagtgc 180
tttggaatt ccaaagtact cagtggagag aggtgtttca ggagccgtag agccagatcg 240
tcatc atg tct gca ttg tgg ctg ctg ctg ggc ctc ctt gcc ctg atg 287

Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met

1 5 10

gac ttg tct gaa agc agc aac tgg gga tgc tat gga aac atc caa agc 335

Asp Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser

15 20 25 30

ctg gac acc cct gga gca tct tgt ggg att gga aga cgt cac ggc ctg 383

Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly Leu

35 40 45

aac tac tgt gga gtt cgt gct tct gaa agg ctg gct gaa ata gac atg 431

Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile Asp Met

50 55 60

cca tac ctc ctg aaa tat caa ccc atg atg caa acc att ggc caa aag 479

Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile Gly Gln Lys

65 70 75

tac tgc atg gat cct gcc gtg atc gct ggt gtc ttg tcc agg aag tct 527

Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu Ser Arg Lys Ser

80 85 90

ccc ggt gac aaa att ctg gtc aac atg ggc gat agg act agc atg gtg 575

Pro Gly Asp Lys Ile Leu Val Asn Met Gly Asp Arg Thr Ser Met Val

95 100 105 110

cag gac cct ggc tct caa gct ccc aca tcc tgg att agt gag tct cag 623

Gln Asp Pro Gly Ser Gln Ala Pro Thr Ser Trp Ile Ser Glu Ser Gln

115 120 125

gtt tcc cag aca act gaa gtt ctg act act aga atc aaa gaa atc cag 671

Val Ser Gln Thr Thr Glu Val Leu Thr Thr Arg Ile Lys Glu Ile Gln

130	135	140	
agg agg ttt cca acc tgg acc cct gac cag tac ctg aga ggt gga ctc			719
Arg Arg Phe Pro Thr Trp Thr Pro Asp Gln Tyr Leu Arg Gly Gly Leu			
145	150	155	
tgt gcc tac agt ggg ggt gct ggc tat gtc cga agc agc cag gac ctg			767
Cys Ala Tyr Ser Gly Gly Ala Gly Tyr Val Arg Ser Ser Gln Asp Leu			
160	165	170	
agc tgt gac ttc tgc aat gat gtc ctt gca cga gcc aag tac ctc aag			815
Ser Cys Asp Phe Cys Asn Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys			
175	180	185	190
aga cat ggc ttc taacatctca gatgaaaccc aagaccatga tcacatatgc agc			870
Arg His Gly Phe			
ctcaaagtgt acacagataa aactagccaa gggcacctgt aactgggaat ctgagtttga			930
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<210> 29
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gatggtgagg catcatgcta gggagctgag ctctgacctt cctgctgggt gattctccac	180
ctctgggctg ctagatctac ttcctggatg ccgtgaagat cctcatgt atg aaa	234

Met Lys

1

atg aag tcc cag gca acc atg att tgc tgc tta gtg ttc ttt ctg tcc	282	
Met Lys Ser Gln Ala Thr Met Ile Cys Cys Leu Val Phe Phe Leu Ser		
5	10	15
aca gaa tgt tcc cac tat aga tcc aag att cac cta aaa agc tat agt	330	
Thr Glu Cys Ser His Tyr Arg Ser Lys Ile His Leu Lys Ser Tyr Ser		

20	25	30	
gaa gtg gcc aac cac atc ctc gac aca gca gcc att tca aac tgg gct			378
Glu Val Ala Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn Trp Ala			
35	40	45	50
ttc att ccc aac aaa aat gcc agc tcg gat ttg ttg cag tca gtg aat			426
Phe Ile Pro Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn			
55	60	65	
ttg ttt gcc aga caa ctc cac atc cac aat aat tct gag aac att gtg			474
Leu Phe Ala Arg Gln Leu His Ile His Asn Asn Ser Glu Asn Ile Val			
70	75	80	
aat gaa ctc ttc att cag aca aaa ggg ttt cac atc aac cat aat acc			522
Asn Glu Leu Phe Ile Gln Thr Lys Gly Phe His Ile Asn His Asn Thr			
85	90	95	
tca gag aaa agc ctc aat ttc tcc atg agc atg aac aat acc aca gaa			570
Ser Glu Lys Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu			
100	105	110	
gat atc tta gga atg gta cag att ccc agg caa gag cta agg aag ctg			618
Asp Ile Leu Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg Lys Leu			
115	120	125	130
tgg cca aat gca tcc caa gcc att agc ata gct ttc cca acc ttg ggg			666
Trp Pro Asn Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr Leu Gly			
135	140	145	
gct atc ctg aga gaa gcc cac ttg caa aat gtg agt ctt ccc aga cag			714
Ala Ile Leu Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro Arg Gln			
150	155	160	
gta aat ggt ctg gtg cta tca gtg gtt tta cca gaa agg ttg caa gaa			762
Val Asn Gly Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu			
165	170	175	
atc ata ctc acc ttc gaa aag atc aat aaa acc cgc aat gcc aga gcc			810
Ile Ile Leu Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala			
180	185	190	
cag tgt gtt ggc tgg cac tcc aag aaa agg aga tgg gat gag aaa gcg			858

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Gly Cys Pro Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr Glu Pro	
375 380 385	
gag aac ggc tac atg aga cct gag gcc tgt tgg ctt aac tgg gac aat	1434
Glu Asn Gly Tyr Met Arg Pro Glu Ala Cys Trp Leu Asn Trp Asp Asn	
390 395 400	
acc aaa gcc ctt tta gca ttt gcc atc ccg gcg ttc gtc att gtg gct	1482
Thr Lys Ala Leu Leu Ala Phe Ala Ile Pro Ala Phe Val Ile Val Ala	
405 410 415	
gta aat ctg att gtg gtt ttg gtt gtt gct gtc aac act cag agg ccc	1530
Val Asn Leu Ile Val Val Leu Val Val Ala Val Asn Thr Gln Arg Pro	
420 425 430	
tct att ggc agt tcc aag tct cag gat gtg gtc ata att atg agg atc	1578
Ser Ile Gly Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met Arg Ile	
435 440 445 450	
agc aaa aat gtt gcc atc ctc act cca ctg ctg gga ctg acc tgg ggt	1626
Ser Lys Asn Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly	
455 460 465	
ttt gga ata gcc act ctc ata gaa ggc act tcc ttg acg ttc cat ata	1674
Phe Gly Ile Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe His Ile	
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Ile Phe Ala Leu Leu Asn Ala Phe Gln Gly Phe Phe Ile Leu Leu Phe	
485 490 495	
gga acc att atg gat cac aag ata aga gat gct ttg agg atg agg atg	1770
Gly Thr Ile Met Asp His Lys Ile Arg Asp Ala Leu Arg Met Arg Met	
500 505 510	
tct tca ctg aag ggg aaa tcg agg gca gct gag aat gca tca cta ggc	1818
Ser Ser Leu Lys Gly Lys Ser Arg Ala Ala Glu Asn Ala Ser Leu Gly	
515 520 525 530	
cca acc aat gga tct aaa tta atg aat cgt caa gga tgaaatgctg ccccat	1870
Pro Thr Asn Gly Ser Lys Leu Met Asn Arg Gln Gly	

535

540

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cagcccgaag cagccagacc agcccctgag cctcccgggt gctggcagct gtc atg 176

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Met

1

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ggg cta ccc tgg ggg cag cct cac cta ggg ctg cag atg ctc ctc ctg 224
Gly Leu Pro Trp Gly Gln Pro His Leu Gly Leu Gln Met Leu Leu Leu

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5

10

15

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gcg ttg aac tgt ctc cgg ccc agc ctg agc ctg gag ctg gtg ccc tac 272
Ala Leu Asn Cys Leu Arg Pro Ser Leu Ser Leu Glu Leu Val Pro Tyr

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20

25

30

41

aca cca cag ata aca gct tgg gac ctg gaa ggg aag gtc aca gcc acc 320
 Thr Pro Gln Ile Thr Ala Trp Asp Leu Glu Gly Lys Val Thr Ala Thr
 35 40 45
 acc ttc tcc ctg gag cag ccg cgc tgt gtc ttc gat ggg ctt gcc agc 368
 Thr Phe Ser Leu Glu Gln Pro Arg Cys Val Phe Asp Gly Leu Ala Ser
 50 55 60 65
 gcc agc gat acc gtc tgg ctc gtg gtg gcc ttc agc aat gcc tcc agg 416
 Ala Ser Asp Thr Val Trp Leu Val Val Ala Phe Ser Asn Ala Ser Arg
 70 75 80
 ggc ttc cag aac ccg gag aca ctg gct gac att ccg gcc tcc cca cag 464
 Gly Phe Gln Asn Pro Glu Thr Leu Ala Asp Ile Pro Ala Ser Pro Gln
 85 90 95
 ctg ctg acc gat ggc cac tac atg acg ctg ccc ctg tct ccg gac cag 512
 Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Pro Asp Gln
 100 105 110
 ctg ccc tgt ggc gac ccc atg gcg ggc agc gga ggc gcc ccc gtg ctg 560
 Leu Pro Cys Gly Asp Pro Met Ala Gly Ser Gly Gly Ala Pro Val Leu
 115 120 125
 cgg gtg ggc cat gac cac ggc tgc cac cag cag ccc ttc tgc aac gcg 608
 Arg Val Gly His Asp His Gly Cys His Gln Gln Pro Phe Cys Asn Ala
 130 135 140 145
 ccc ctc cct ggc cct gga ccc tat cgg gtg aag ttc ctc ctg atg gac 656
 Pro Leu Pro Gly Pro Gly Pro Tyr Arg Val Lys Phe Leu Leu Met Asp
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 Thr Arg Gly Ser Pro Arg Ala Glu Thr Lys Trp Ser Asp Pro Ile Thr
 165 170 175
 ctc cac caa ggg aag acc ccc gga tcc atc gac acc tgg cca ggg cgg 752
 Leu His Gln Gly Lys Thr Pro Gly Ser Ile Asp Thr Trp Pro Gly Arg
 180 185 190
 cga agt ggc agc atg atc gtc att acc tcc atc ctc tct tct ctg gcc 800
 Arg Ser Gly Ser Met Ile Val Ile Thr Ser Ile Leu Ser Ser Leu Ala

195	200	205	
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Gly Leu Leu Leu Leu Ala Phe Leu Ala Ala Ser Thr Met Arg Phe Ser			
210	215	220	225
agc ctg tgg tgg ccg gag gag gcc ccg gag cag ctg cgg atc ggc tcc			896
Ser Leu Trp Trp Pro Glu Glu Ala Pro Glu Gln Leu Arg Ile Gly Ser			
230	235	240	
ttc atg ggc aag cgc tac atg acc cac cac atc cca ccc agc gag gcc			944
Phe Met Gly Lys Arg Tyr Met Thr His His Ile Pro Pro Ser Glu Ala			
245	250	255	
gcc aca ctg ccg gtg ggc tgc aag cct ggc ctg gac ccc ctc ccc agc			992
Ala Thr Leu Pro Val Gly Cys Lys Pro Gly Leu Asp Pro Leu Pro Ser			
260	265	270	
ctc agc ccc tagcctggcc tctttgcatg gggctggggg agatggggc			1040
Leu Ser Pro			
275			
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